

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: October 30, 2006, 15:30:46 ; Search time 168.997 Seconds
(without alignments)
2479.522 Million cell updates/sec

Title: US-10-578-992-2_COPY_19_471

Perfect score: 2349

Sequence: 1 QASATAYLTKEASAKNGV.....RNGFTCASWGAKGVSTSCST 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2341 ⁶	99.7	579	2	Q12596_9APHY	Q12596 athelia rol
2	1738.5	74.0	570	2	Q33CE4_9APHY	Q33ce4 fomitopsis
3	1560	66.4	571	2	Q9P4C5_LENED	Q9p4c5 lentinula e
4	1357.5	57.8	631	2	Q4WIT7_ASPFU	Q4wit7 aspergillus
5	1348.5	57.4	639	2	Q76L97_ASPAW	Q76l97 aspergillus
6	1347.5	57.4	639	1	AMYG_ASPSH	P22832 aspergillus
7	1347	57.3	640	1	AMYG_ASPAW	P69327 aspergillus
8	1347	57.3	640	1	AMYG_ASPNG	P69328 aspergillus
9	1346	57.3	640	2	Q6DNH5_ASPNG	Q6dnh5 aspergillus
10	1336	56.9	640	2	Q6DUY5_ASPFI	Q6duy5 aspergillus
11	1332	56.7	639	1	AMYG_ASPKA	P23176 aspergillus
12	1330.5	56.6	612	2	Q3HLW7_ASPOR	Q3hlw7 aspergillus
13	1324.5	56.4	612	1	AMYG_ASPOR	P36914 aspergillus
14	1320	56.2	639	2	Q12537_ASPAW	Q12537 aspergillus
15	1307.5	55.7	626	1	AMYG_NEUCR	P14804 neurospora
16	1305.5	55.6	639	2	Q870G8_ASPNG	Q870g8 aspergillus
17	1283	54.6	618	2	Q9CLV4_TALEM	Q9clv4 talaromyces
18	1252	53.3	661	2	Q5AWC3_EMENI	Q5awc3 aspergillus
19	1229	52.3	617	2	Q58HNI_THELA	Q58hni thermomyces
20	1202.5	51.2	613	2	Q4WFY4_ASPFU	Q4wfy4 aspergillus
21	1193	50.8	620	2	Q12623_ASACO	Q12623 humicola gr
22	1189.5	50.6	582	2	Q4HUN2_GIBZE	Q4hun2 gibberella
23	1188	50.6	493	2	Q2ULP9_ASPOR	Q2ulp9 aspergillus
24	1182	50.3	493	2	Q5984C_ASPOR	Q5984c aspergillus
25	1171	49.9	488	2	Q76KF7_PENCH	Q76kf7 penicillium
26	1126	47.9	620	2	Q599K8_TRIHA	Q599k8 trichoderma
27	1125	47.9	616	1	AMYG_HORRE	Q03045 hormoconis
28	1117.5	47.6	579	2	Q41930_GIBZE	Q41930 gibberella
29	1076.5	45.8	1264	2	Q5AS26_EMENI	Q5as26 aspergillus
30	888	37.8	547	2	Q4P749_USTMA	Q4p749 ustilago ma
31	779.5	33.2	609	2	Q8J0P8_MUCCI	Q8j0p8 mucor circi

32	764.5	32.5	604	2	Q2VC81_RHIOR	Q2vc81 rhizopus or
33	746.5	31.8	604	1	AMYG_RHIOR	P07683 rhizopus or
34	745.5	31.7	579	2	Q7Z7X9_RHIOR	Q2z7x9 rhizopus or
35	713.5	30.4	480	2	Q2VER8_RHIOR	Q2ver8 rhizopus or
36	694.5	29.6	450	1	AMYG_SCHPO	O60087 schizosacch
37	676.5	28.8	577	2	Q55SB7_CRYNE	Q55sb7 cryptococcu
38	664.5	28.3	577	2	Q5KGR4_CRYNE	Q5kgr4 cryptococcu
39	631.5	26.9	624	1	AMYG_AEXAD	P42042 arkula aden
40	630	26.8	519	1	AMYH_SACFI	P26989 saccharomyc
41	625.5	26.6	602	2	Q6C6Y8_YARLI	Q6c6y8 yarrowia li
42	623	26.5	519	1	AMYG_SACFI	P08017 saccharomyc
43	611.5	26.0	515	2	Q8TFE5_SACFI	O8tfe5 saccharomyc
44	565.5	24.1	564	2	Q5AJ73_CANAL	Q5aj73 candida alb
45	538.5	22.9	545	2	Q6BY56_DEBHA	Q6by56 debaryomyc

ALIGNMENTS

RESULT 1

Q12596_9APHY PRELIMINARY; PRT; 579 AA.
AC Q12596;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Glucoamylase G2 (EC 3.2.1.3).
OS Athelia rolfsii.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Athelia.
OX NCBI_TaxID=39291;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AHU9627;
RX MEDLINE=96158471; PubMed=8597548; DOI=10.1007/s002530050581;
RA Nagasaka Y., Muraki N., Kimura A., Suto M., Yokota A., Tomita F.;
RT "Cloning of Corticium rolfsii glucoamylase cDNA and its expression in
RT Saccharomycetes cerevisiae.";
RL Appl. Microbiol. Biotechnol. 44:451-458 (1995).
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EMBL; D49448; BAA08436.1; -; mRNA.
DR HSSP; P04064; 1GAI.
DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR008291; Glucamylase_SBD.
DR InterPro; IPR011613; Glyco_hydro_15; 1.
DR InterPro; IPR000165; Glyco_hydro_15.
DR InterPro; IPR002044; Glyco_hydro_s_bd.
DR InterPro; IPR012343; Glyco_trans_sub.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF00723; Glyco_hydro_15; 1.
DR PIRSF; PIRSF001031; Glu-a-glycd_SBD; 1.
DR PRINTS; PD00736; GLHYDLASE15.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
KW Glycosidase; Hyalolase.
SQ SEQUENCE 579 AA; 61549 MW; FF56D83F9D1A9EC9 CRC64;

Query Match Score 2341; DB 2; Length 579;
Best Local Similarity 99.8%; Pred. No. 1.6e-162;
Matches 452; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	QASATAYLTKEASAKNGVLCNIGSQCMSEGAISGIVIASPKTSDDYLYTTTRDSSL	60
DB	19	QASATAYLTKEASAKNGVLCNIGSQCMSEGAISGIVIASPKTSDDYLYTTTRDSSL	78
QY	61	VFKMLIDQYNTGLDITLRLTLDIFVSAEATIQOTSNPSGTVSTGGLGEPKKNIDETAFTG	120
DB	79	VFKMLIDQYNTGLDITLRLTLDIFVSAEATIQOTSNPSGTVSTGGLGEPKKNIDETAFTG	138

QY 121 AWGRPQDGPALRATAIMTYATYLYNNGNTSYVTWTLWPIIKLDLDYNSDWNQTTFDLW 180
 DB 139 AWGRPQDGPALRATAIMTYATYLYNNGNTSYVTWTLWPIIKLDLDYNSDWNQTTFDLW 198
 QY 181 BEVDSSPFTTAVQHRALVQGAAPATLIGQTSASTYSATAPSLICFLQSYWNTNGYWT 240
 DB 199 BEVDSSPFTTAVQHRALVQGAAPATLIGQTSASTYSATAPSLICFLQSYWNTNGYWT 258
 QY 241 NTGGRSGKDANTILASHTFDASAGCSAATSQPCSDVALANLKYVYVDSFRSIYTIINS 300
 DB 259 NTGGRSGKDANTILASHTFDASAGCSAATSQPCSDVALANLKYVYVDSFRSIYTIINS 318
 QY 301 SSTSGVATGRYPEDSYNGNPNWYLCTLAVALAEQLYDALIWKAAAGELNVTSLAPFQPD 360
 DB 319 SSTSGVATGRYPEDSYNGNPNWYLCTLAVALAEQLYDALIWKAAAGELNVTSLAPFQPD 378
 QY 361 SSITAGTYASSSSVYTSLSIDIQAFADRFVDIVAKYTPSSGFLSEYDKSTGAQDSANL 420
 DB 379 SSITAGTYASSSSVYTSLSIDIQAFADRFVDIVAKYTPSSGFLSEYDKSTGAQDSANL 438
 QY 421 TWSYAAAATAYOARNGFTGASGAKGVSTSCST 453
 DB 439 TWSYAAAATAYOARNGFTGASGAKGVSTSCST 471

RESULT 2
 Q33CE4 9APHY PRELIMINARY; PRT; 570 AA.
 AC Q33CE4
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Glucoamylase.
 GN Name=glu
 OS Fomitopsis palustris
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Fomitopsid.
 OX NCBI_TaxID=184125;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FFPRI 0507;
 RA Yoon J., Igarashi K., Kajisa T., Samejima M.;
 RT "Characterization and Molecular Cloning of Glycoside Hydrolase Family
 RT 15 Glucoamylase from the brown-rot basidiomycete Fomitopsis
 RT palustris."
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 DR EMBL; AB239766; BAE47183.1; -; mRNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
 SQ SEQUENCE 570 AA; 61247 MW; E7CE3BAC56A702B CRC64;

Query Match 74.0%; Score 1738.5; DB 2; Length 570;
 Best Local Similarity 73.6%; Pred. No. 1.8e-118
 Matches 332; Conservative 46; Mismatches 72; Indels 1; Gaps 1;

QY 3 ASATAYLTKEASAVKNGVLNIGSGOGCMSEGAISGIVIASPKTSYDLYTWTRDSSLVF 62
 DB 19 SNVTSYISTETPLAKAGLANIGDPSLSGAKSGIVIASPSTVNPOTLYTWTRDSSLVF 78
 QY 63 KMLIDQYTNGLDITLRLTIDFVSAAETIQOTSNPSTVSTGGLGEPKFNIDETAFTCAW 122
 DB 79 KALIDQFVSGEDTLGLPLIDFTSAQAIQQIDNPSGVSSTGGLGEPKFNIDETAFTCAW 138
 QY 123 GRPQDGPALRATAIMTYATYLYNNGNTSYVTWTLWPIIKLDLDYNSDWNQTTFDLWEE 182
 DB 139 GRPQDGPALRATAIMTYATYLYNNGNTSYVTWTLWPIIKLDLDYNSDWNQTTFDLWEE 198
 QY 183 VDSSEFFTTAVQHRALVQGAAPATLIGQTSASTYSATAPSLICFLQSYWNTNGYWTAN 240

DB 199 VDSSEFFTTAVQHRALREGITFANLIGTSDVSNWETQADLLCFLQSYWNTDLYMTAN 258
 QY 242 TGGGRSGKDANTILASHTFDASAGCSAATSQPCSDVALANLKYVYVDSFRSIYTIINS 301
 DB 259 TGGGRSGKDANTILASHTFDPEAGCDDVTFCPCSDKALSNLKYVYVDSFRSIYTIINS 318
 QY 302 STSGVATGRYPEDSYNGNPNWYLCTLAVALAEQLYDALIWKAAAGELNVTSLAPFQPD 361
 DB 319 SDAVATGRYPEDSYNGNPNWFLTLAAAEQLYDALIWNQAQSLNVTSTSLAPFQPD 378
 QY 362 SITAGTYASSSSVYTSLSIDIQAFADRFVDIVAKYTPSSGFLSEYDKSTGAQDSANL 421
 DB 379 SVTAGTYASSGDEFTLTLSAIQTADGFVELIAKTYPSGSLSEYDKSTGAQDSANL 438
 QY 421 WSYAAAATAYOARNGFTGASGAKGVSTSCS 452
 DB 439 WSYAAAATAYOARNGFTGASGAKGVSTSCS 469

RESULT 3
 Q9P4C5 LENED PRELIMINARY; PRT; 571 AA.
 AC Q9P4C5
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Glucoamylase.
 OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Lentinula.
 OX NCBI_TaxID=5353;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20292826; PubMed=10831434;
 RX DOI=10.1128/AEM.66.6.2531-2535.2000;
 RA Zhao J., Chen Y.H., Kwan H.S.;
 RT "Molecular cloning, characterization, and differential expression of a
 RT glucoamylase gene from the basidiomycetous fungus Lentinula edodes."
 RL Appl. Environ. Microbiol. 66:2531-2535(2000).
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 CC
 DR EMBL; AF220541; AAF75523.1; -; mRNA.
 DR HSSP; P04064; 1GAI.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
 DR InterPro; IPR008291; Glucoamylase_SBD.
 DR InterPro; IPR011613; Glyco_hydro_15rel.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR002044; Glyco_hydro_s_bd.
 DR InterPro; IPR012343; Glyco_trans_sub.
 DR Pfam; PF00686; CEM_20; 1.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PRINTS; PIRSF001031; Glu-a-glucsd_SBD; 1.
 DR PRINTS; PR00736; GLHYDLASE15.
 DR ProDom; PD001568; Glyco_hydro_CBD; 1.
 SQ SEQUENCE 571 AA; 61162 MW; A1BD1ECC848B97FF CRC64;

Query Match 66.4%; Score 1560; DB 2; Length 571;
 Best Local Similarity 64.7%; Pred. No. 2.1e-105;
 Matches 292; Conservative 64; Mismatches 95; Indels 0; Gaps 0;

QY 1 OSATAYLTKEASAVKNGVLNIGSGOGCMSEGAISGIVIASPKTSYDLYTWTRDSSLV 60
 DB 18 QSSVIDAYASESPLAKASMLANIGPSKSGSAGFSGIVIASPTENPDLYTWTRDSSLV 77
 QY 61 VFKMLIDQYTNGLDITLRLTIDFVSAAETIQOTSNPSTVSTGGLGEPKFNIDETAFTG 120
 DB 78 TFQIIIDQFTLGLDITLRAEIDNVGAQAIQQIPNPSGDITTTGGLGEPKFNIDETAFTG 137

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OM protein - protein search, using sw model

Run on: October 30, 2006, 15:30:46 ; Search time 216.003 Seconds
(without alignments):
2479.522 Million cell updates/sec

Title: US-10-578-992-2
Perfect score: 3001
Sequence: 1 MFRSLALACAVASVSQAQ.....REITTPASCTYTKDWDSE 579

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2993 ³	99.7	579	2	Q12596_9APHY	Q12596 athelia rol
2	2044	68.1	570	2	Q33CE4_9APHY	Q33CE4 fomitopsis
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4	1592	53.0	631	2	Q4WIT7_ASPFU	Q4WIT7 aspergillus
5	1576.5	52.5	639	1	AMYG_ASPSH	P22832 aspergillus
6	1576.5	52.5	639	2	Q76L97_ASPAW	Q76L97 aspergillus
7	1576	52.5	640	1	AMYG_ASPAW	P69127 aspergillus
8	1576	52.5	640	1	AMYG_ASPNG	P69328 aspergillus
9	1575	52.5	640	2	Q6DNH5_ASPNG	Q6DNH5 aspergillus
10	1565	52.1	640	2	Q6DUY5_ASPFI	Q6DUY5 aspergillus
11	1558.5	51.9	639	1	AMYG_ASPKA	P23176 aspergillus
12	1553.5	51.8	639	2	Q12537_ASPAW	Q12537 aspergillus
13	1534.5	51.1	639	2	Q870G8_ASPNG	Q870G8 aspergillus
14	1530	51.0	612	2	Q3HLW7_ASPOR	Q3HLW7 aspergillus
15	1524	50.8	612	1	AMYG_ASPOR	P14804 aspergillus
16	1499.5	50.0	626	1	AMYG_NEUCR	P14804 neurospora
17	1473.5	49.1	618	2	Q9C1V4_TALEM	Q9C1V4 talaromyces
18	1463.5	48.8	661	2	Q5AWC8_EMENI	Q5AWC8 aspergillus
19	1411.5	47.0	617	2	Q5HNI1_THELA	Q5HNI1 thermomyces
20	1353	45.1	582	2	Q4HUN2_GIBZE	Q4HUN2 gibberella
21	1332.5	44.4	613	2	Q4WFY4_ASPFU	Q4WFY4 aspergillus
22	1330.5	44.3	620	2	Q12623_9ASCO	Q12623 humicola gr
23	1310	43.7	616	1	AMYG_HORRE	Q03045 hormoconis
24	1294.5	43.1	579	2	Q41930_GIBZE	Q41930 gibberella
25	1204.5	40.1	1264	2	Q5AS26_EMENI	Q5AS26 aspergillus
26	1200.5	40.0	493	2	Q2ULP9_ASPOR	Q2ULP9 aspergillus
27	1195	39.8	620	2	Q599K8_TRIHA	Q599K8 trichoderma
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31	779.5	26.0	609	2	Q8J0P8_MUCCI	Q8J0P8 mucor circi

32	765.5	25.5	604	2	Q2VC81_RHIOR	Q2VC81 rhizopus or
33	747.5	24.9	604	1	AMYG_RHIOR	P07683 rhizopus or
34	746.5	24.9	579	2	Q7Z7X9_RHIOR	Q7Z7X9 rhizopus or
35	715.5	23.8	480	2	Q2VER8_RHIOR	Q2VER8 rhizopus or
36	696.5	23.2	450	1	AMYG_SCHPO	O60087 schizosacch
37	683.5	22.8	577	2	Q55SB7_CRYNE	Q55SB7 cryptococcu
38	671.5	22.4	577	2	Q5KGR4_CRYNE	Q5KGR4 cryptococcu
39	633.5	21.1	624	1	AMYG_ARDAD	P42042 arxula aden
40	631	21.0	519	1	AMVH_SACFI	P26989 saccharomyc
41	626	20.9	602	2	Q6C6Y8_YARLI	Q6C6Y8 yarrowia li
42	624	20.8	519	1	AMYG_SACFI	P08017 saccharomyc
43	615.5	20.5	515	2	Q8TFB5_SACFI	Q8TFB5 saccharomyc
44	565.5	18.8	564	2	Q5AJ73_CANAL	Q5AJ73 candida alb
45	538.5	17.9	545	2	Q6BY56_DEBHA	Q6BY56 debaryomyce

ALIGNMENTS

RESULT 1

Q12596_9APHY PRELIMINARY; PRT; 579 AA.
AC Q12596;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Glucoamylase G2 (EC 3.2.1.3).
OS Athelia rolfsii.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Athelia.
OX NCBI_TaxID=39291;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AH9627;
RA Nagasaka Y., Muraki N., Kimura A., Suto M., Yokota A., Tomita F.;
RT "Cloning of Corticium rolfsii glucoamylase cDNA and its expression in
Saccharomyces cerevisiae";
RL Appl. Microbiol. Biotechnol. 44:451-458 (1995).

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EMBL; D49448; BAA08436.1; -; mRNA.
DR HSSP; P04064; IGA1.
DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR InterPro; IPR008291; Glucamylase_SBD.
DR InterPro; IPR011613; Glyco_hydro15rel.
DR InterPro; IPR000165; Glyco_hydro15.
DR InterPro; IPR002044; Glyco_hydro_s_bd.
DR InterPro; IPR012343; Glyco_trans_sub.
DR Pfam; PF00686; CBM_20; 1.
DR PIRSF; PIRSF001031; Glu-a-glucsd_SBD; 1.
DR PRINTS; PR00736; GLHYDLASE15.
DR ProDom; PD001568; Glyco_hydro_CBD; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 579 AA; 61549 MW; FF56D83F9D1A9EC9 CRC64;

Query Match 99.7%; Score 2993; DB 2; Length 579;
Best Local Similarity 99.8%; Pred. No. 1.2e-190;
Matches 578; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MFRSLALACAVASVSQAQSAATAYLTKEBAVAKNGVLCNIGSGQCMSEGAISGIVIAS	60
DB	1	MFRSLALACAVASVSQAQSAATAYLTKEBAVAKNGVLCNIGSGQCMSEGAISGIVIAS	60
QY	61	PSKTSPLYTWTRDSSILVFQMLIDQYTNGLDITLTILIDFVSAEATIQOTSNPSGTVS	120
DB	61	PSKTSPLYTWTRDSSILVFQMLIDQYTNGLDITLTILIDFVSAEATIQOTSNPSGTVS	120

QY 121 TGLGPKFNIDETAFTGAWGRPQDGPALRATAIMTYATLYNNGNTSYVNTLWPIIK 180
 DB 121 TGLGPKFNIDETAFTGAWGRPQDGPALRATAIMTYATLYNNGNTSYVNTLWPIIK 180
 QY 181 LDLYVNSDMNQTTFDLWEEDSSSFFTTAVQHRALVQGAAPATLIGOTSASTYSATAP 240
 DB 181 LDLYVNSDMNQTTFDLWEEDSSSFFTTAVQHRALVQGAAPATLIGOTSASTYSATAP 240
 QY 241 SILCFLOSQYWNQYNTANTGGSGKDKANTILASIHFTFDSAGCSAATSQPCSDVALAN 300
 DB 241 SILCFLOSQYWNQYNTANTGGSGKDKANTILASIHFTFDSAGCSAATSQPCSDVALAN 300
 QY 301 LKVVYVDSFRSYIYNTINGSISSGTGATGRYPEDSYNGNPNWYLCTLAVALYDYLIVWKA 360
 DB 301 LKVVYVDSFRSYIYNTINGSISSGTGATGRYPEDSYNGNPNWYLCTLAVALYDYLIVWKA 360
 QY 361 AGEINVTSSVLAFFQFQDSSITAGTYASSSSVYTSLSIDIOAFADFFVDIVAKYTPSSGF 420
 DB 361 AGEINVTSSVLAFFQFQDSSITAGTYASSSSVYTSLSIDIOAFADFFVDIVAKYTPSSGF 420
 QY 421 LSEQYDKSTGQDSANLITWYAAAITAYQARNGFTGASWAKGVSTSCSTGATSPGSSS 480
 DB 421 LSEQYDKSTGQDSANLITWYAAAITAYQARNGFTGASWAKGVSTSCSTGATSPGSSS 480
 QY 481 GSVEVTFDVTATVYGVNIYITGDSVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540
 DB 481 GSVEVTFDVTATVYGVNIYITGDSVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540
 QY 541 YKYVNDGSTVIMWEDALSINREITTPASCTYTEKTDWDS 579
 DB 541 YKYVNDGSTVIMWEDALSINREITTPASCTYTEKTDWDS 579

RESULT 2

Q33CE4_9APHY PRELIMINARY; PRT; 570 AA.
 AC Q33CE4;
 DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
 DT 06-DEC-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Glucoamylase.
 GN Name=gla;
 OS Fomitopsis palustris.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Fomitopsis.
 OX NCBI_TaxID=186125;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FPFRI 0507;
 RA Yoon J., Igarashi K., Kajisa T., Samejima M.;
 RT "Characterization and Molecular Cloning of Glycoside Hydrolase Family
 15 Glucoamylase from the brown-rot basidiomycete Fomitopsis
 palustris.";
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 CC EMBL; AB239766; BAB47183.1; -; mRNA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:0005976; P:polysaccharide metabolism; IEA.
 SQ SEQUENCE 570 AA; 61247 MW; E77CE3BAC56A702B CRC64;

Query Match 68.1%; Score 2044; DB 2; Length 570;
 Best Local Similarity 69.3%; Pred. No. 1.9e-127;
 Matches 399; Conservative 63; Mismatches 104; Indels 10; Gaps 5;
 QY 3 RSLALAAACAVASQAQASATAYLTKEASVAVKNGVLNITGSGQCMSEGAISGIVASPS 62
 DB 2 RLSLSFVLGLVAFAAQSNVTSYISTETPLAKAGVLNITGSGSLGAKSGIVIASPS 60
 QY 63 KTSPEVLYITWTRDSSLVFKMLIDQYNTGLTLTLIDEFVSABEATIQTSNFSGVSTG 122

DB 61 TVNPDYLYTTRDSSLTFKALIDQFVSGEDDTLGLDDFTSAQAIIQQIDNPGSVSTG 120
 QY 123 GLGEPKFNIDETAFTGAWGRPQDGPALRATAIMTYATLYNNGNTSYVNTLWPIIK 182
 DB 121 GLGEPKFNIDETAFTGAWGRPQDGPALRATAIMTYATLYNNGNTSYVNTLWPIIK 180
 QY 183 LDYVNSDMNQTTFDLWEEDSSSFFTTAVQHRALVQGAAPATLIGOTSASTYSATAPSI 242
 DB 181 LDYVNSDMNQTTFDLWEEDSSSFFTTAVQHRALVQGAAPATLIGOTSASTYSATAPSI 240
 QY 243 LCFLOSQYWNQYNTANTGGSGKDKANTILASIHFTFDSAGCSAATSQPCSDVALANL 301
 DB 241 LCFLOSQYWNQYNTANTGGSGKDKANTILASIHFTFDSAGCSAATSQPCSDVALANL 300
 QY 302 LKVVYVDSFRSYIYNTINGSISSGTGATGRYPEDSYNGNPNWYLCTLAVALYDYLIVWKA 361
 DB 301 LKVVYVDSFRSYIYNTINGSISSGTGATGRYPEDSYNGNPNWYLCTLAVALYDYLIVWKA 360
 QY 362 AGEINVTSSVLAFFQFQDSSITAGTYASSSSVYTSLSIDIOAFADFFVDIVAKYTPSSGF 421
 DB 361 AGEINVTSSVLAFFQFQDSSITAGTYASSSSVYTSLSIDIOAFADFFVDIVAKYTPSSGF 420
 QY 422 LSEQYDKSTGQDSANLITWYAAAITAYQARNGFTGASWAKGVSTSCSTGATSPGSSS 481
 DB 421 LSEQYDKSTGQDSANLITWYAAAITAYQARNGFTGASWAKGVSTSCSTGATSPGSSS 474
 QY 482 GSVEVTFDVTATVYGVNIYITGDSVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 540
 DB 475 GSVEVTFDVTATVYGVNIYITGDSVSELGNWTPANGVALSSANYPTWSATIALPADTTIQ 534
 QY 541 YKYVNDGSTVIMWEDALSINREITTPASCTYTEKTDW 576
 DB 535 YKYVNDGSTVIMWEDALSINREITTPASCTYTEKTDW 569

RESULT 3

Q9P4CS_LENED PRELIMINARY; PRT; 571 AA.
 AC Q9P4CS;
 DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 23.
 DE Glucoamylase.
 OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Tricholomataceae; Lentinula.
 OX NCBI_TaxID=5353;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20292826; PubMed=10831434;
 RX DOI=10.1128/AEM.66.6.2531-2535.2000;
 RA Zhao J., Chen Y.H., Kwan H.S.;
 RT "Molecular cloning, characterization, and differential expression of a
 glucoamylase gene from the basidiomycetous fungus Lentinula edodes";
 RL Appl. Environ. Microbiol. 66:2531-2535(2000).
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 CC
 CC EMBL; AF220541; AAF75523.1; -; mRNA.
 DR HSSP; P04064; IGAI.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:000272; P:polysaccharide catabolism; IEA.
 DR InterPro; IPR008231; Glucamylase_SBD.
 DR InterPro; IPR011613; Glyco_hydro15rel.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR002044; Glyco_hydro_s bd.
 DR InterPro; IPR012343; Glyco_trans_sub.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR FIRSF001031; Glu-a-gicsd_SBD; 1.